

SEQUENCE LISTING

5 <110> Vanderbilt University
 Balser, Jeffrey R.
 George, Alfred L.
 Roden, Dan M.

10 <120> HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK

15 10 <130> 1242-49

20 15 <150> 60/244,340
 <151> 2000-10-30

25 20 <160> 7

30 25 <170> PatentIn version 3.1

35 30 20 <210> 1
 <211> 1857
 <212> DNA
 <213> Homo sapiens

40 35 25 <220>
 <221> CDS
 <222> (1)..(1422)
 <223> n is any nucleotide

45 40 30 <220>
 <221> misc_feature
 <222> (1)..(1857)
 <223> n is any nucleotide

50 45 35 <400> 1

55 50 40 atg gcg cag cta gag ggt tac tgt ttc tcg gcc gcc ttg agc tgt acc 48
 Met Ala Gln Leu Glu Gly Tyr Cys Phe Ser Ala Ala Leu Ser Cys Thr
 1 5 10 15

60 55 45 ttt tta gtg tcc tgc ctc ctc ttc tcc gcc ttc agc cgg gcg ctg cga 96
 Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg
 20 25 30

65 60 50 gag ccc tac atg gac gag atc ttc cac ctg cct cag gcg cag cgc tac 144
 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
 35 40 45

70 65 55 tgt gag ggc cat ttc tcc ctt tcc cag tgg gat ccc atg att act aca 192
 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
 50 55 60

75 70 65 tta cct ggc ttg tac ctg gtg tca gtt gga gtg gtc aaa cct gcc att 240
 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
 75 80

10	tgg atc ttt gga tgg tct gaa cat gtt gtc tgc tcc att ggg atg ctc Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu 85 90 95	288
5	aga ttt gtt aat ctt ctc ttc agt gtt ggc aac ttc tat tta cta tat Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr 100 105 110	336
10	ttg ctt ttc cac aag gta caa ccc aga aac aag gct gcc tca agt atc Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile 115 120 125	384
15	cag aga gtc ttg tca aca tta aca cta gca gta ttt cca aca ctt tat Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr 130 135 140	432
20	ttt ttt aac ttc ctt tat tat aca gaa gca gga tct atg ttt ttt act Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr 145 150 155 160	480
25	ctt ttt gca tat ttg atg tgt ctt tat gga aat cat aaa act tca gcc Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala 165 170 175	528
30	tcc ctt gga ttt tgt ggc ttc atg ttt cgg caa aca aat atc atc tgg Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp 180 185 190	576
35	gct gtc ttc tgt gca ggg aat gtc att gca caa aag tta act gag gct Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala 195 200 205	624
40	tgg aaa act gag cta caa aag aag gaa gac aga ctt cca cct att aaa Trp Lys Thr Glu Leu Gln Lys Glu Asp Arg Leu Pro Pro Ile Lys 210 215 220	672
45	gga cca ttt gca gaa ttc aga aaa att ctt cag ttt ctt ttg gct tat Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr 225 230 235 240	720
50	tcc atg tcc ttt aaa aac ttg agt atg ctt ttc tgt ttg act tgg ccc Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro 245 250 255	768
55	tac atc ctt ctg gga ttt ctg ttt tgt gct ttt gta gta gtt aat ggt Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Asn Gly 260 265 270	816
55	gga att gtt att ggc gat cgg agt agt cat gaa gcc tgt ctt cat ttt Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe 275 280 285	864
55	cct caa cta ttc tac ttt tca ttt act ctc ttt ttt tct ttt cct Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro 290 295 300	912

cat ctc ctg tct cct agc aaa att aag act ttt ctt tcc tta gtt tgg	960
His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp	
305 310 315 320	
5 aaa cat gga att ctg ttt ttg gtg gtt acc tta gtc tct gtg ttt tta	1008
Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu	
325 330 335	
10 gtt tgg aaa ttc act tat gct cat aaa tac ttg cta gca gac aat aga	1056
Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg	
340 345 350	
15 cat tat act ttc tat gtg tgg aaa aga gtt ttt caa aga tat gca att	1104
His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile	
355 360 365	
20 ctg aaa tat ttg tta gtt cca gcc tat ata ttt gct ggt tgg agt ata	1152
Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile	
370 375 380	
25 gct gac tca ttg aaa tca aag cca att ttt tgg aat tta atg ttt ttc	1200
Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe	
385 390 395 400	
30 ata tgc ttg ttc att gtt ata gtt cct cag aaa ctg ctg gaa ttt cgt	1248
Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg	
405 410 415	
35 tac ttc att tta cct tat gtc att tat agg ctt aac ata act ctg cct	1296
Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro	
420 425 430	
40 ccc aca tcc aga ctt gtt tgt gaa ctg agt tgc tat gca att gtt aat	1344
Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn	
435 440 445	
45 ttc ata act ttt tac atc ttt ctg aac aag act ttt cag tgg cca aat	1392
Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn	
450 455 460	
50 agt cag gac att caa agg ttt atg tgg taa tatcagtgtat attttgaact	1442
Ser Gln Asp Ile Gln Arg Phe Met Trp	
465 470	
45 gtaaaaaatgg acttaataat agaccatttc tacaaaagaac aactgaatag gngggaaaaca	1502
tggaaatttct ttttaggtgca gtgggtgtct tcaaattaca ttagttttt taatatatat	1562
55 tttaaacata tgtaagaaat taagtggcaa agaactggaa aagcttaaga cctgcttcaa	1622
angcctgaat aatggaaaaa taaaanwngtt tncagatatac tcatacgct cnnnnknatgn	1682
tggcccytmn caangcttgg gaatgkttnn wntgnataag ttnattaaan ctgggnntgc	1742
55 tnnmwatnac tttnnnkncca nccwnnnwac natgnnnntan nnantattta caaaggtcag	1802
gtgatattct tgactgaaaaa gtgctctnaa cataaaaagta aatatgngcc ncaaa	1857

5 <210> 2
 <211> 473
 <212> PRT
 <213> Homo sapiens
 10 <220>
 <221> misc_feature
 <222> (1)..(1857)
 <223> n is any nucleotide
 <400> 2
 15 Met Ala Gln Leu Glu Gly Tyr Cys Phe Ser Ala Ala Leu Ser Cys Thr
 1 5 10 15
 Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg
 20 25 30
 20 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
 35 40 45
 25 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
 50 55 60
 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
 65 70 75 80
 30 Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu
 85 90 95
 Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr
 100 105 110
 35 Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile
 115 120 125
 40 Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr
 130 135 140
 Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr
 145 150 155 160
 45 Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala
 165 170 175
 Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp
 180 185 190
 50 Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala
 195 200 205
 Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys
 210 215 220
 55 Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr
 225 230 235 240

Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro
245 250 255

5 Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly
260 265 270

Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe
275 280 285

10 Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro
290 295 300

His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp
15 305 310 315 320

Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu
325 330 335

20 Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg
340 345 350

His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile
25 355 360 365

Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile
370 375 380

Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe
30 385 390 395 400

Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg
405 410 415

35 Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro
420 425 430

Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn
40 435 440 445

Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn
450 455 460

Ser Gln Asp Ile Gln Arg Phe Met Trp
45 465 470

50 <210> 3
<211> 1159
<212> PRT
<213> Homo sapiens

<400> 3

55 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp
1 5 10 15

Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala
20 25 30

Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe
5 35 40 45

Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys
50 55 60

10 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala
65 70 75 80

Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile
85 90 95

15 Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val
100 105 110

20 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
115 120 125

Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp
130 135 140

25 Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala
145 150 155 160

Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg
165 170 175

30 Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly
180 185 190

35 Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu
195 200 205

Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly
210 215 220

40 Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro
225 230 235 240

Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu
245 250 255

45 Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser
260 265 270

50 Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile
275 280 285

Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala Ser
290 295 300

55 Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser
305 310 315 320

Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile
325 330 335

5 Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro
340 345 350

Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His
355 360 365

10 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val
370 375 380

Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr Ile
385 390 395 400

15 Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu
405 410 415

Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu
20 420 425 430

Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala
435 440 445

25 Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe Ile
450 455 460

Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn Glu
465 470 475 480

30 Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys Gly
485 490 495

Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile
35 500 505 510

Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala Arg
515 520 525

40 Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu
530 535 540

Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile
545 550 555 560

45 Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu Gln
565 570 575

50 Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp Gln
580 585 590

Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile Lys
595 600 605

55 Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser
610 615 620

Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile Phe
625 630 635 640

5 Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe
645 650 655

Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg
660 665 670

10 Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His Gln
675 680 685

Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala
690 695 700

15 Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe
705 710 715 720

20 Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser Leu
725 730 735

Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu Arg
740 745 750

25 Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr
755 760 765

Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser Arg
770 775 780

30 Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu Gly
785 790 795 800

35 Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro Gly
805 810 815

Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys
820 825 830

40 Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu Phe
835 840 845

Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg Asp
850 855 860

45 Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly Gly
865 870 875 880

50 Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr Asp
885 890 895

Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly Arg
900 905 910

55 Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly
915 920 925

Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu
930 935 940

5 Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser
945 950 955 960

Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp
965 970 975

10 Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser
980 985 990

Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln
995 1000 1005

15 Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu
1010 1015 1020

Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val
20 1025 1030 1035

Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu
1040 1045 1050

25 Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln
1055 1060 1065

Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr
1070 1075 1080

30 Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser
1085 1090 1095

35 Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln
1100 1105 1110

Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro
1115 1120 1125

40 Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu Gly
1130 1135 1140

Ala Leu Thr Ser Gln Pro Leu His Arg His Gly Ser Asp Pro Gly
1145 1150 1155

45 Ser

50 <210> 4
<211> 732
<212> DNA
<213> Homo sapiens

55 <220>
<221> CDS
<222> (74) .. (445)
<223>

<400> 4

5 caaatccaga aaagatccgt tttcctaacc ttgttcgcct attttattat ttaaattgca 60
gcaggaggga agc atg tct act tta tcc aat ttc aca cag acg ctg gaa 109
Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu
1 5 10

10 gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157
Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln
15 20 25

15 aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205
Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
30 35 40

20 aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253
Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
45 50 55 60

25 tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301
Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg
65 70 75

30 cg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349
Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp
80 85 90

35 cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397
Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
95 100 105

40 acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc tga 445
Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
110 115 120

45 taaggagaa aggaccaag ctaacatctg acgtccagac atgaagagat gccagtgc 505
cgaggcaaat ccaaattgtc tttgcttaga agaaagttag ttccttgctc tctgttgaga 565
attttcatgg agattatgtg gttggccaat aaagatagat gacatttcaa tctcagtgat 625
ttatgcttgc ttgttggagc aatattttgt gctgaagacc tctttactt tccgggcaag 685
tgaatgtcat tttaatcaat atcaatgtatg aaaataaagc caaattt 732

50 <210> 5
<211> 123
<212> PRT
<213> Homo sapiens

55 <400> 5

Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu Asp Val Phe Arg
1 5 10 15

Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln Asn Thr Thr Ala
5 20 25 30

Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr
35 40 45

10 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile
50 55 60

Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
65 70 75 80

15 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr
85 90 95

20 Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu
100 105 110

Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
115 120

25 <210> 6

<211> 21

<212> DNA

<213> Synthetic

30 <400> 6

55 tttcaaagat atgcaattct g

21

35 <210> 7

<211> 20

<212> DNA

<213> Synthetic

40 <400> 7

75 aagtccattt ttacagttca

20